

RAW SEQUENCE LISTING

**The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.**

Application Serial Number: 10/594,293
Source: IFWP
Date Processed by STIC: 10/05/2006

ENTERED



IFWP

RAW SEQUENCE LISTING

DATE: 10/05/2006

PATENT APPLICATION: US/10/594,293

TIME: 09:43:33

Input Set : A:\PB60806seqlist.txt

Output Set: N:\CRF4\10052006\J594293.raw

5 <110> APPLICANT: Glaxo Group Limited
 7 Ellis, Jonathan H
 9 Eon-Duval, Alexandre
 11 Germaschewski, Volker
 13 Plumptre, Christopher
 15 Rapson, Nicholas Timothy
 17 West, Michael Robert
 21 <120> TITLE OF INVENTION: Immunoglobulins
 25 <130> FILE REFERENCE: PB60806
 C--> 29 <140> CURRENT APPLICATION NUMBER: US/10/594,293
 C--> 31 <141> CURRENT FILING DATE: 2006-09-26
 35 <150> PRIOR APPLICATION NUMBER: GB 0407197.3
 37 <151> PRIOR FILING DATE: 2004-03-30
 41 <150> PRIOR APPLICATION NUMBER: GB 0407193.2
 43 <151> PRIOR FILING DATE: 2004-03-30
 47 <160> NUMBER OF SEQ ID NOS: 65
 51 <170> SOFTWARE: PatentIn version 3.1
 55 <210> SEQ ID NO: 1
 57 <211> LENGTH: 5
 59 <212> TYPE: PRT
 61 <213> ORGANISM: Mus sp.
 65 <400> SEQUENCE: 1
 67 Asn Tyr Gly Val His
 68 1 5
 71 <210> SEQ ID NO: 2
 73 <211> LENGTH: 16
 75 <212> TYPE: PRT
 77 <213> ORGANISM: Mus sp.
 81 <400> SEQUENCE: 2
 83 Val Ile Trp Arg Gly Gly Ser Thr Asp Tyr Asn Ala Ala Phe Met Ser
 84 1 5 10 15
 87 <210> SEQ ID NO: 3
 89 <211> LENGTH: 12
 91 <212> TYPE: PRT
 93 <213> ORGANISM: Mus sp.
 97 <400> SEQUENCE: 3
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 100 1 5 10
 103 <210> SEQ ID NO: 4
 105 <211> LENGTH: 10
 107 <212> TYPE: PRT
 109 <213> ORGANISM: Mus sp.
 113 <400> SEQUENCE: 4

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115 Ser Gly Ser Ser Ser Val Ser Tyr Met Tyr
116 1 5 10
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121 <211> LENGTH: 7
123 <212> TYPE: PRT
125 <213> ORGANISM: Mus sp.
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131 Asp Thr Ser Asn Leu Ala Ser
132 1 5
135 <210> SEQ ID NO: 6
137 <211> LENGTH: 9
139 <212> TYPE: PRT
141 <213> ORGANISM: Mus sp.
145 <400> SEQUENCE: 6
147 Gln Gln Trp Ser Ser Tyr Pro Pro Thr
148 1 5
151 <210> SEQ ID NO: 7
153 <211> LENGTH: 120
155 <212> TYPE: PRT
157 <213> ORGANISM: Mus sp.
161 <400> SEQUENCE: 7
163 Gln Val Gln Leu Lys Gln Ser Gly Pro Gly Leu Val Gln Pro Ser Gln
164 1 5 10 15
167 Ser Leu Ser Ile Thr Cys Thr Val Ser Gly Phe Ser Leu Thr Asn Tyr
168 20 25 30
171 Gly Val His Trp Val Arg Gln Ser Pro Gly Lys Gly Leu Glu Trp Leu
172 35 40 45
175 Gly Val Ile Trp Arg Gly Gly Ser Thr Asp Tyr Asn Ala Ala Phe Met
176 50 55 60
179 Ser Arg Leu Ser Ile Thr Lys Asp Asn Ser Arg Ser Gln Val Phe Phe
180 65 70 75 80
183 Lys Met Asn Ser Leu Gln Ala Asp Asp Thr Ala Ile Tyr Tyr Cys Ala
184 85 90 95
187 Lys Ser Pro Asn Ser Asn Phe Tyr Trp Tyr Phe Asp Val Trp Gly Thr
188 100 105 110
191 Gly Thr Thr Val Thr Val Ser Ser
192 115 120
195 <210> SEQ ID NO: 8
197 <211> LENGTH: 106
199 <212> TYPE: PRT
201 <213> ORGANISM: Mus sp.
205 <400> SEQUENCE: 8
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208 1 5 10 15
211 Glu Lys Val Thr Met Thr Cys Ser Gly Ser Ser Ser Val Ser Tyr Met
212 20 25 30
215 Tyr Trp Tyr Gln Glu Lys Pro Gly Ser Ser Pro Arg Leu Leu Ile Glu
216 35 40 45
219 Asp Thr Ser Asn Leu Ala Ser Gly Val Pro Ala Arg Phe Ser Gly Ser

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220      50                      55                      60
223 Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile Ser Arg Met Glu Ala Glu
224 65                      70                      75                      80
227 Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Ser Tyr Pro Pro Thr
228                      85                      90                      95
231 Phe Gly Ser Gly Thr Lys Leu Glu Ile Lys
232                      100                      105
235 <210> SEQ ID NO: 9
237 <211> LENGTH: 120
239 <212> TYPE: PRT
241 <213> ORGANISM: Artificial sequence
245 <220> FEATURE:
247 <223> OTHER INFORMATION: VH domain (humanised, B3)
249 <400> SEQUENCE: 9
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252 1                      5                      10                      15
255 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Ser Leu Thr Asn Tyr
256                      20                      25                      30
259 Gly Val His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
260                      35                      40                      45
263 Ala Val Ile Trp Arg Gly Gly Ser Thr Asp Tyr Asn Ala Ala Phe Met
264                      50                      55                      60
267 Ser Arg Phe Thr Ile Ser Lys Asp Asn Ser Lys Asn Thr Leu Tyr Leu
268 65                      70                      75                      80
271 Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
272                      85                      90                      95
275 Lys Ser Pro Asn Ser Asn Phe Tyr Trp Tyr Phe Asp Val Trp Gly Arg
276                      100                      105                      110
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280                      115                      120
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285 <211> LENGTH: 106
287 <212> TYPE: PRT
289 <213> ORGANISM: Artificial sequence
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295 <223> OTHER INFORMATION: VL domain (humanised, L2)
297 <400> SEQUENCE: 10
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300 1                      5                      10                      15
303 Glu Arg Ala Thr Leu Ser Cys Ser Gly Ser Ser Ser Val Ser Tyr Met
304                      20                      25                      30
307 Tyr Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile Glu
308                      35                      40                      45
311 Asp Thr Ser Asn Leu Ala Ser Gly Ile Pro Ala Arg Phe Ser Gly Ser
312                      50                      55                      60
315 Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser Asn Leu Glu Pro Glu
316 65                      70                      75                      80
319 Asp Phe Ala Val Tyr Tyr Cys Gln Gln Trp Ser Ser Tyr Pro Pro Thr
320                      85                      90                      95

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329 <211> LENGTH: 450
331 <212> TYPE: PRT
333 <213> ORGANISM: Artificial sequence
337 <220> FEATURE:
339 <223> OTHER INFORMATION: Heavy chain (humanised)
341 <400> SEQUENCE: 11
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344 1          5          10          15
347 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Ser Leu Thr Asn Tyr
348          20          25          30
351 Gly Val His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
352          35          40          45
355 Ala Val Ile Trp Arg Gly Gly Ser Thr Asp Tyr Asn Ala Ala Phe Met
356          50          55          60
359 Ser Arg Phe Thr Ile Ser Lys Asp Asn Ser Lys Asn Thr Leu Tyr Leu
360 65          70          75          80
363 Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
364          85          90          95
367 Lys Ser Pro Asn Ser Asn Phe Tyr Trp Tyr Phe Asp Val Trp Gly Arg
368          100          105          110
371 Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
372          115          120          125
375 Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala
376          130          135          140
379 Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser
380 145          150          155          160
383 Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
384          165          170          175
387 Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
388          180          185          190
391 Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys
392          195          200          205
395 Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp
396          210          215          220
399 Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly
400 225          230          235          240
403 Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile
404          245          250          255
407 Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu
408          260          265          270
411 Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
412          275          280          285
415 Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg
416          290          295          300
419 Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
420 305          310          315          320

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423 Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu
424           325           330           335
427 Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr
428           340           345           350
431 Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu
432           355           360           365
435 Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
436~ 370           375           380
439 Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val
440 385           390           395           400
443 Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp
444           405           410           415
447 Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
448           420           425           430
451 Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
452           435           440           445
455 Gly Lys
456 450
459 <210> SEQ ID NO: 12
461 <211> LENGTH: 213
463 <212> TYPE: PRT
465 <213> ORGANISM: Artificial sequence
469 <220> FEATURE:
471 <223> OTHER INFORMATION: Light chain (humanised)
473 <400> SEQUENCE: 12
475 Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
476 1           5           10           15
479 Glu Arg Ala Thr Leu Ser Cys Ser Gly Ser Ser Ser Val Ser Tyr Met
480           20           25           30
483 Tyr Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile Glu
484           35           40           45
487 Asp Thr Ser Asn Leu Ala Ser Gly Ile Pro Ala Arg Phe Ser Gly Ser
488           50           55           60
491 Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser Asn Leu Glu Pro Glu
492 65           70           75           80
495 Asp Phe Ala Val Tyr Tyr Cys Gln Gln Trp Ser Ser Tyr Pro Pro Thr
496           85           90           95
499 Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg Thr Val Ala Ala Pro
500           100          105          110
503 Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr
504           115          120          125
507 Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys
508           130          135          140
511 Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu
512 145          150          155          160
515 Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser
516           165          170          175
519 Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala
520           180          185          190

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VERIFICATION SUMMARY

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L:29 M:270 C: Current Application Number differs, Replaced Current Application Number

L:31 M:271 C: Current Filing Date differs, Replaced Current Filing Date